

PCT

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/786,442

DATE: 03/23/2001
 TIME: 09:45:58

Input Set : A:\991043sequence.txt
 Output Set: N:\CRF3\03232001\I786442.raw

ENTERED

3 <110> APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
 4 TAKAHASHI, Tsuneo
 5 ONO, Mitsuharu
 6 ISHIMARU, Hiroshi
 7 KANNO, Kimiyoshi
 8 TAKAHASHI, Chiaki
 10 <120> TITLE OF INVENTION: Novel receptor protein and method for the diagnosis of an
 11 inflammatory disease by using the same
 13 <130> FILE REFERENCE: 99-1043
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/786,442
 C--> 15 <141> CURRENT FILING DATE: 2001-03-05
 15 <150> PRIOR APPLICATION NUMBER: JP 10-249752
 16 <151> PRIOR FILING DATE: 1998-09-03
 18 <150> PRIOR APPLICATION NUMBER: JP 11-070800
 19 <151> PRIOR FILING DATE: 1999-03-16
 21 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04801
 22 <151> PRIOR FILING DATE: 1999-09-03
 24 <160> NUMBER OF SEQ ID NOS: 12
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 1014
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)...(1011)
 35 <400> SEQUENCE: 1
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 37 Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr Ser Asp Leu
 38 1 5 10 15
 39 tcg gac cgc cct gtg gac tgc ctg gat ggc gcc tgc ctg gcc atc gac 96
 40 Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
 41 20 25 30
 42 ccg ctg cgc gtg gcc ccg ctc cca ctg tat gcc gcc atc ttc ctg gtg 144
 43 Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
 44 35 40 45
 45 ggg gtg ccg ggc aat gcc atg gtg gcc tgg gtg gct ggg aag gtg gcc 192
 46 Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
 47 50 55 60
 48 cgc cgg agg gtg ggt gcc acc tgg ttg ctc cac ctg gcc gtg gcg gat 240
 49 Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
 50 65 70 75 80
 51 ttg ctg tgc tgt ttg tct ctg ccc atc ctg gca gtg ccc att gcc cgt 288
 52 Leu Leu Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
 53 85 90 95
 54 gga ggc cac tgg ccg tat ggt gca gtg ggc tgg cgg gcg ctg ccc tcc 336
 55 Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
 56 100 105 110

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57 atc atc ctg ctg acc atg tat gcc aqc gtc ctg ctc ctg gca gct ctc	384
58 Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Ala Ala Leu	
59 115 120 125	
60 agt gcc gac ctc tgc ttc ctg gct ctc ggg cct gcc tgg tgg tct acg	432
61 Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr	
62 130 135 140	
63 gtt cag cgg gcg tgc ggg gtg cag gtg gcc tgt ggg gca gcc tgg aca	480
64 Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr	
65 145 150 155 160	
66 ctg gcc ttg ctg ctc acc gtg ccc tcc gcc atc tac cac cgg ctg cac	528
67 Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His	
68 165 170 175	
69 cag gag cac ttc cca gcc cgg ctg cag tgt gtg gtg gac tac ggc ggc	576
70 Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly	
71 180 185 190	
72 tcc tcc agc acc gag aat ggc gtg act gcc atc cgg ttt ctt ttt ggc	624
73 Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly	
74 195 200 205	
75 ttc ctg ggg ccc ctg gtg gcc gtg gac tgc cac agt gcc ctc ctg	672
76 Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu	
77 210 215 220	
78 tgc tgg gca gcc cga cgc tgc cgg cgg ctg ggc aca gcc att gtg gtg	720
79 Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val	
80 225 230 235 240	
81 ggg ttt ttt gtc tgc tgg gca ccc tac cac ctc ctg ggg ctg gtg ctc	768
82 Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly Leu Val Leu	
83 245 250 255	
84 act gtg gcg gcc ccg aac tcc gca ctc ctg gcc agg gcc ctg cgg gct	816
85 Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala	
86 260 265 270	
87 gaa ccc ctc atc gtg ggc ctt gcc ctc gct cac agc tgc ctc aat ccc	864
88 Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro	
89 275 280 285	
90 atg ctc ttc ctg tat ttt ggg agg gct caa ctc cgc cgg tca ctg cca	912
91 Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro	
92 290 295 300	
93 gct gcc tgt cac tgg gcc ctg agg gag tcc cag ggc cag gac gaa agt	960
94 Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser	
95 305 310 315 320	
96 gtg gac agc aag aaa tcc acc agc cat gac ctg gtc tgg gag atg gag	1008
97 Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu	
98 325 330 335	
99 gtg tag	1014
100 Val	
103 <210> SEQ ID NO: 2	
104 <211> LENGTH: 337	
105 <212> TYPE: PRT	
106 <213> ORGANISM: Homo sapiens	
108 <400> SEQUENCE: 2	

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109 Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr Ser Asp Leu
110   1           5          10          15
111 Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
112           20          25          30
113 Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
114           35          40          45
115 Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
116           50          55          60
117 Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
118   65           70          75          80
119 Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
120           85          90          95
121 Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
122           100         105         110
123 Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu Ala Ala Leu
124           115         120         125
125 Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr
126           130         135         140
127 Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr
128   145           150         155         160
129 Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His
130           165         170         175
131 Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly
132           180         185         190
133 Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly
134           195         200         205
135 Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu
136           210         215         220
137 Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val
138   225           230         235         240
139 Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly Leu Val Leu
140           245         250         255
141 Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala
142           260         265         270
143 Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro
144           275         280         285
145 Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro
146           290         295         300
147 Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser
148   305           310         315         320
149 Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu
150           325         330         335
151 Val
154 <210> SEQ ID NO: 3
155 <211> LENGTH: 1287
156 <212> TYPE: DNA
157 <213> ORGANISM: Homo sapiens
159 <400> SEQUENCE: 3
160 cctgtgtgcc acgtgctgga caaatcttaa ctccctcaagg actccccaaa ccagagacac    60

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161 caggaggctg aatggggAAC gattctgtca gctacqagta tggggattac agcgaccctc 120
162 cggaccgccc tgtggactgc ctggatggcg ctcgcctggc catcgaccgg ctgcgcgtgg 180
163 ccccgctccc actgtatgcc gccatcttcc tgggggggt gccggcaat gccatgggg 240
164 cctggggcgc tggaaagggt gcccggcgga ggggtgggtc caccgtgggg ctccacccgg 300
165 ccgtggcggg tttgtgtc tgggtgtc tgeccatctt ggcagtggcc attggccgtg 360
166 gaggccactg gccgtatggt qcagtgggt gtcggcggt gcccggccatc atccgtgtc 420
167 ccatgtatgc cagcgctctg ctctggcag ctctcagtgc cgacccctgc ttccctggc 480
168 tcgggcctgc ctgggtgtc acggttcagc gggcgtggg ggtgcagggt gcctgtgggg 540
169 cagcctggac actggccttg ctgtcaccgc tgcctccgc catctaccgc cggctgcacc 600
170 aggagcaccc cccagcccg otgcagtgtg tggggacta cgggggttcc tccagcaccc 660
171 agaatgcgtt gactggccatc cgggttctt tggcttctt gggggccctg gtggccgtgg 720
172 ccagctgcca cagtggccctc ctgtgtggg cagccggacg ctggccggcc ctgggcacag 780
173 ccattgtgtt ggggtttttt gtctgtggg caccctacca cctgtgggg ctgggtgtca 840
174 ctgtggcgcc cccgaaactgc gcactctgg cccggccctt gggggctgaa cccctccatcg 900
175 tggccctgc ctcgtccatc agctgttca atccatgtt ctgcgtgtat tttggggagg 960
176 ctcacttccg cccgttactg ccaactgtt gtcacttggc ccttggggag tccccaggccc 1020
177 aggacgaaaag tggacacgc aaaaatcca ccaagccatga cctggctcg gagatgggg 1080
178 ttaggtgtgg agagacattt tgggtgtta tcttcttata tcatttcaca agactggctt 1140
179 caggcatatc tggatccagg agctcaatgg tggcttcatt tatttccttc cttcatcaa 1200
180 cagatatcca tcatgttca gctatgttca aggctttttt aggactaga gatatacgag 1260
181 tgacaaaaac agacacaaat cctggccc 1287
184 <210> SEQ ID NO: 4
185 <211> LENGTH: 1287
186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 4
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191 acatagaacg tgcgtatgg atatctgtt aatgaaggaa ggaataaaat gaagacatca 120
192 tttaggtctt ggatccaggat atgcgttcaag ccaggctgtt gaaatggat aagaagatac 180
193 acaccccaaa tggctcttca gcttacacccatc cttatccgg aaccgggttca tggctgggg 240
194 atttcttctt gtcacccactt tcgtcttggc cttggggactc cttcaggccc cagtgtacagg 300
195 cagctggcgat tgaccggcg agttggccccc tcccaaaaata cagaagagc atgggatttg 360
196 ggcagctgtg agcggggcgca agggccacga tgagggttc agcccgccagg gcccggccca 420
197 ggagtggcgaa gttcggggcc gccacaggatc gcaaccggcc cccggggatc taggggtgccc 480
198 agcagacaaa aaaccccccaca acaatggctg tggccacggg cccggccatc cgggctgccc 540
199 agcacaggag ggcactgtgg cagttggccca cggccacccgg gggcccccagg aagccaaaaa 600
200 gaaacccggat ggcagtcacc gcatttctgg tgctggagga gcccggtag tccaccacac 660
201 actgcagccg ggctggaaag tgctcttggt gcaaggccggc gtagatggcg gagggcagg 720
202 tgagcgttca ggcacgttgc caggctggcc cacaggccac ctgcacccccc caccggccgt 780
203 gaaccgttca ccacccaggca ggcccggagag ccaggaaagca gaggttggca ctgagatgt 840
204 ccaggaggcg gacgttggca tatactggca gcaaggatgtt gggggccagg gcccggacac 900
205 ccactgttcc accatggccatgg tggcttccac gggcaatggg cactggccagg atgggatgg 960
206 acaaaacacca cagcaaatcc gccacggccca ggtggagca caaggatggca cccaccctcc 1020
207 ggcggggccac ctcccaaggcc acccaggccca ccatggcattt gcccggccacc cccaccaggaa 1080
208 agatggggcc atacatgggg agcggggccca cccggccagg gtcgtatggcc aggcaggccg 1140
209 catccaggcc gtcacccaggcc cgggttccggaa ggtcgttca atccccatatac tctgtatgt 1200
210 cagaatgttcc ccccaatttca gtcctgggtt tctctgggtt tggggatctt tgaggatgtt 1260
211 agatggcc accacgttcc acacagg 1287
214 <210> SEQ ID NO: 5

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215 <211> LENGTH: 30
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
W--> 220 <221> NAME/KEY: modified base
221 <222> LOCATION: 18
222 <223> OTHER INFORMATION: i
224 <220> FEATURE:
W--> 225 <221> NAME/KEY: modified base
226 <222> LOCATION: 22
227 <223> OTHER INFORMATION: i
229 <220> FEATURE:
W--> 230 <221> NAME/KEY: modified base
231 <222> LOCATION: 24
232 <223> OTHER INFORMATION: i
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Degenerative PCR primer designed based on the seq of conventional
236    7-pass transmembrane receptor proteins which are considered to
237    participate in the proliferation of melanoma
240 <400> SEQUENCE: 5
W> 241 atcttaagct tgaacctngc ctngcdgac 30
244 <210> SEQ ID NO: 6
245 <211> LENGTH: 33
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
W--> 250 <221> NAME/KEY: misc difference
251 <222> LOCATION: 21
252 <223> OTHER INFORMATION: a, g, c or t
254 <220> FEATURE:
W--> 255 <221> NAME/KEY: modified base
256 <222> LOCATION: 22
257 <223> OTHER INFORMATION: i
259 <220> FEATURE:
W--> 260 <221> NAME/KEY: modified base
261 <222> LOCATION: 28
262 <223> OTHER INFORMATION: i
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Degenerative PCR primer designed based on the seq of conventional
266    7-pass transmembrane receptor proteins which are considered to
267    participate in the proliferation of melanoma
269 <400> SEQUENCE: 6
W> 270 cccaaacgaaat tcrttagatsa nhggrrttnav rca 33
273 <210> SEQ ID NO: 7
274 <211> LENGTH: 32
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Synthetic primer used for constructing the recombinant DNA

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VERIFICATION SUMMARY DATE: 03/23/2001
PATENT APPLICATION: US/09/786,442 TIME: 09:45:59

Input Set : A:\991043sequence.txt
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L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:220 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:225 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:230 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:250 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:255 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:260 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6